

### Abstract

A method for selecting epigenetic features includes receiving an epigenetic feature data set for a plurality of epigenetic features of interest. The epigenetic feature data set is grouped in disjoint classes of interest. Epigenetic features of interest and/or combinations of epigenetic features of interest are selected that are relevant for epigenetically-based prediction based on corresponding epigenetic feature data. A new set of epigenetic features of interest is defined based on the relevant epigenetic features of interest and/or combinations of epigenetic features of interest.